

Analysis of 17724 (399 aa)

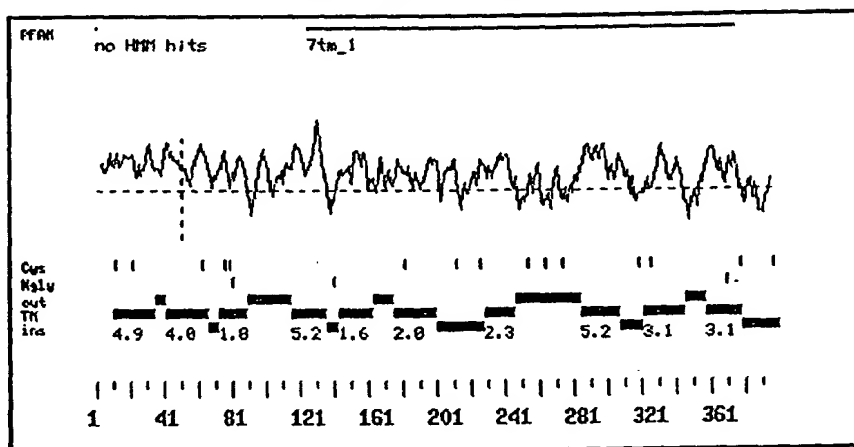


FIG. 1

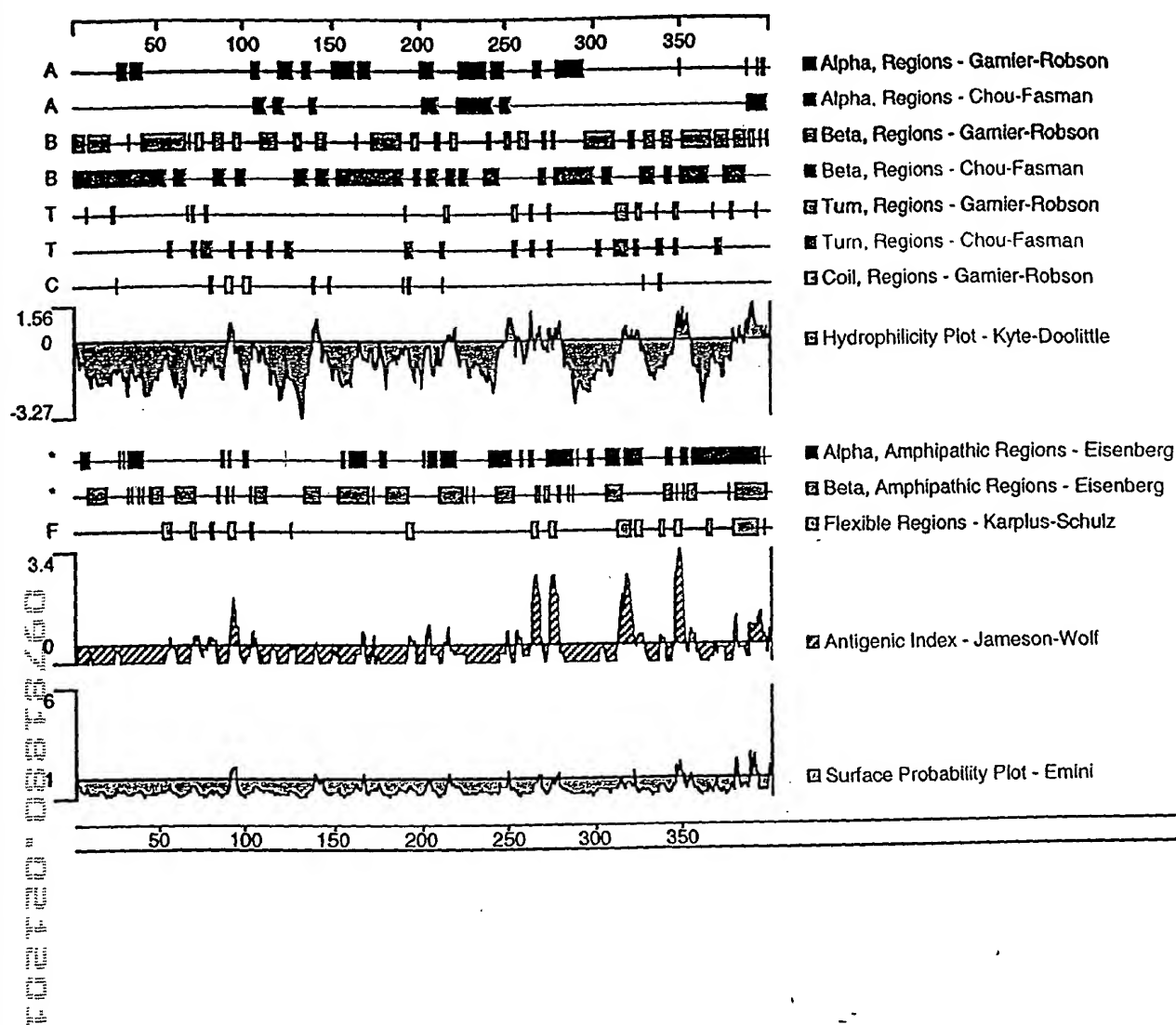


FIG. 2

[illegible]

Model	Description	Score	E-value	N
7tm_1	7 transmembrane receptor (rhodopsin family)	94.1	6.1e-29	1

Parsed for domains:						score	E-value
Model	Domain	seq-f	seq-t	hmm-f	hmm-t		
7tm_1	1/1	125	374	1	259	[1]	6.1e-29

```

Alignments of top-scoring domains:
7tm_1: domain 1 of 1, from 125 to 374: score 94.1, E = 6.1e-29
*--GNLVLvIlvIlrtKkIrtpnifILNLAVALLLfIltpwalyylvg
17724 125 GN ++i+ ++ +ltp++f+N ++ +L++ t +p +l+ +
GNTIIIVMVIADTHLHTPMYFFLGNSLLEILVTMTAVPRMLSDLLV 171

gsedWpfGsaIcKlvtaldvnmmyaSiIlLtaISiDRYLAivhPlryrrr
++++ +C ++ ++ + + +S l Lt ++DR++AI+hPlry ++
17724 172 --PHKVITFTGCMVQVFYFHSLGSTSFILILTMALDRFVAICHPRLRYGT 219

rtsprrrAkvvillvWvIalIlslPpIlfswkvtveegntlnvntvtvCli
++ + + + ++W++ +l +P ++S ++ + +g+ +n+++C+
17724 220 MS-RAMCVQLAGAAWAAFLAMVPT-VLSRAHLDYCHGGV--INHFPCDN 265

dfpeestasvstwlrsyvlIstIvgFlIpIlvlvCvYtrIlrtlr....
+ ++s+ l+++ +l l +l +lv l+ Y+ I+ t+ ++
17724 266 EPLQLQSCSDTRLLEFWDPLMALTFVLSFVLTLSISGYIVTFTVLRlps 315

...kaaktIlvvvvvFvlCWlPyfivIlldtlc.lsiImstCelervlp
++ + a+ ++ ++ + + +l++++ + s ++
17724 316 sscQKAPSTCGSHLTlVfIGYSSTIFLYVRPGKaHS-----VQ 353

tallvtlwLayvNscINPiY+*
+ v+l+ +++ + lNP+I
17724 354 VRKVVAlVTSVLTFFLNPfIL 374

```

17724 Expression in Clinical Lung Samples



17724

17724 Expression in Clinical Angiogenic Samples

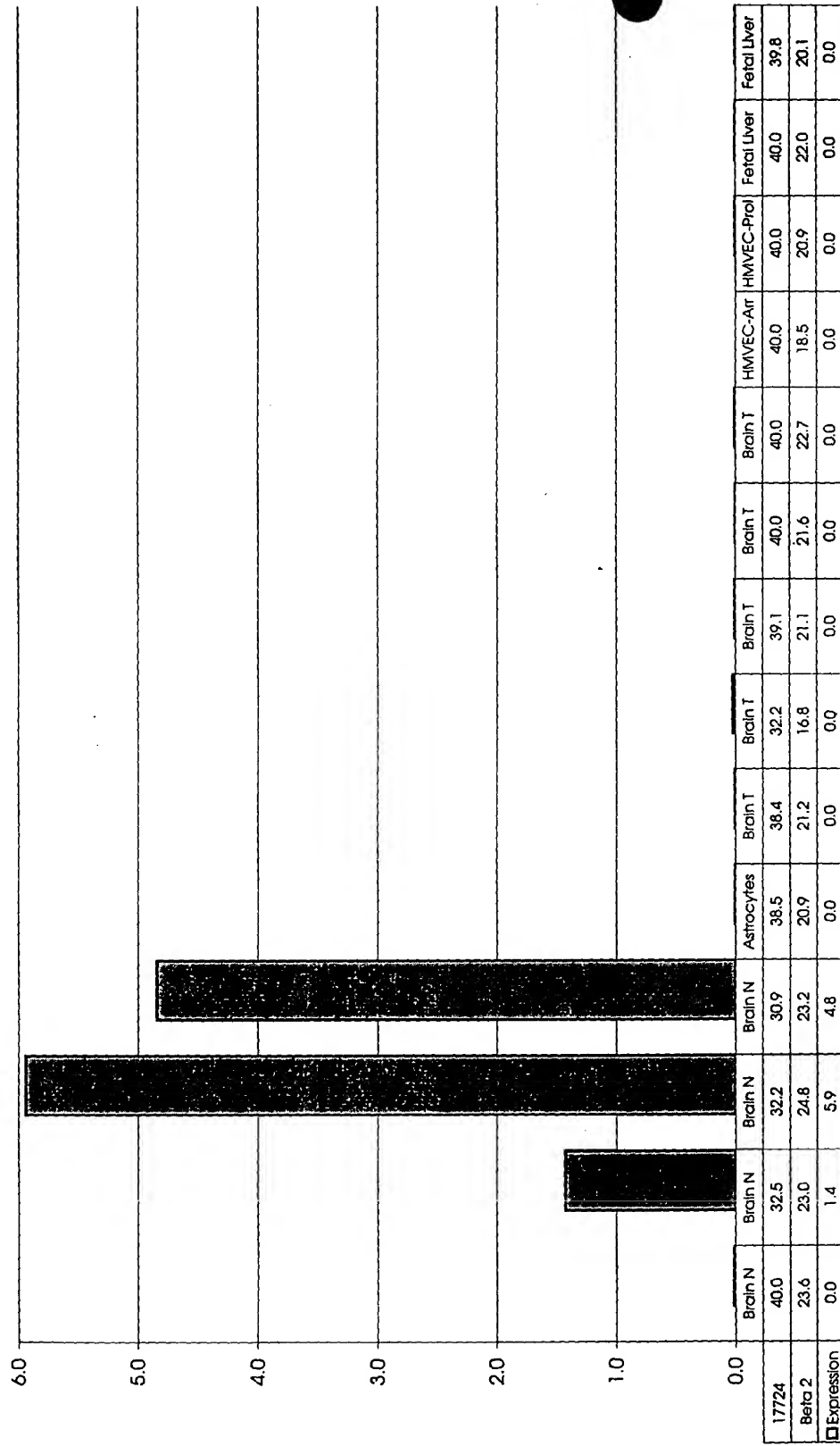


FIG. 5

FOR "333T663"

17724 CV II

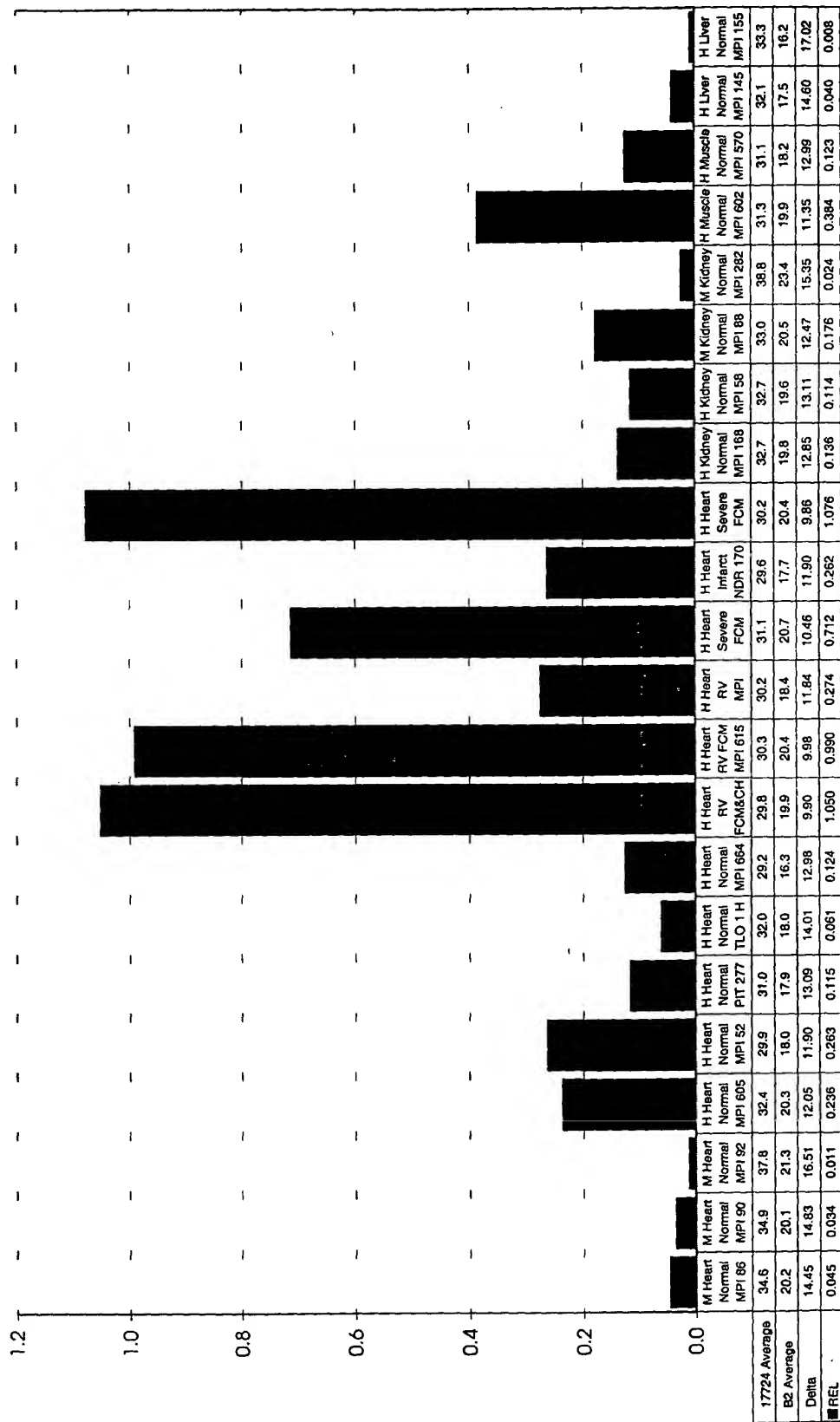


FIG. 6

FIG. 7

17724 CV III

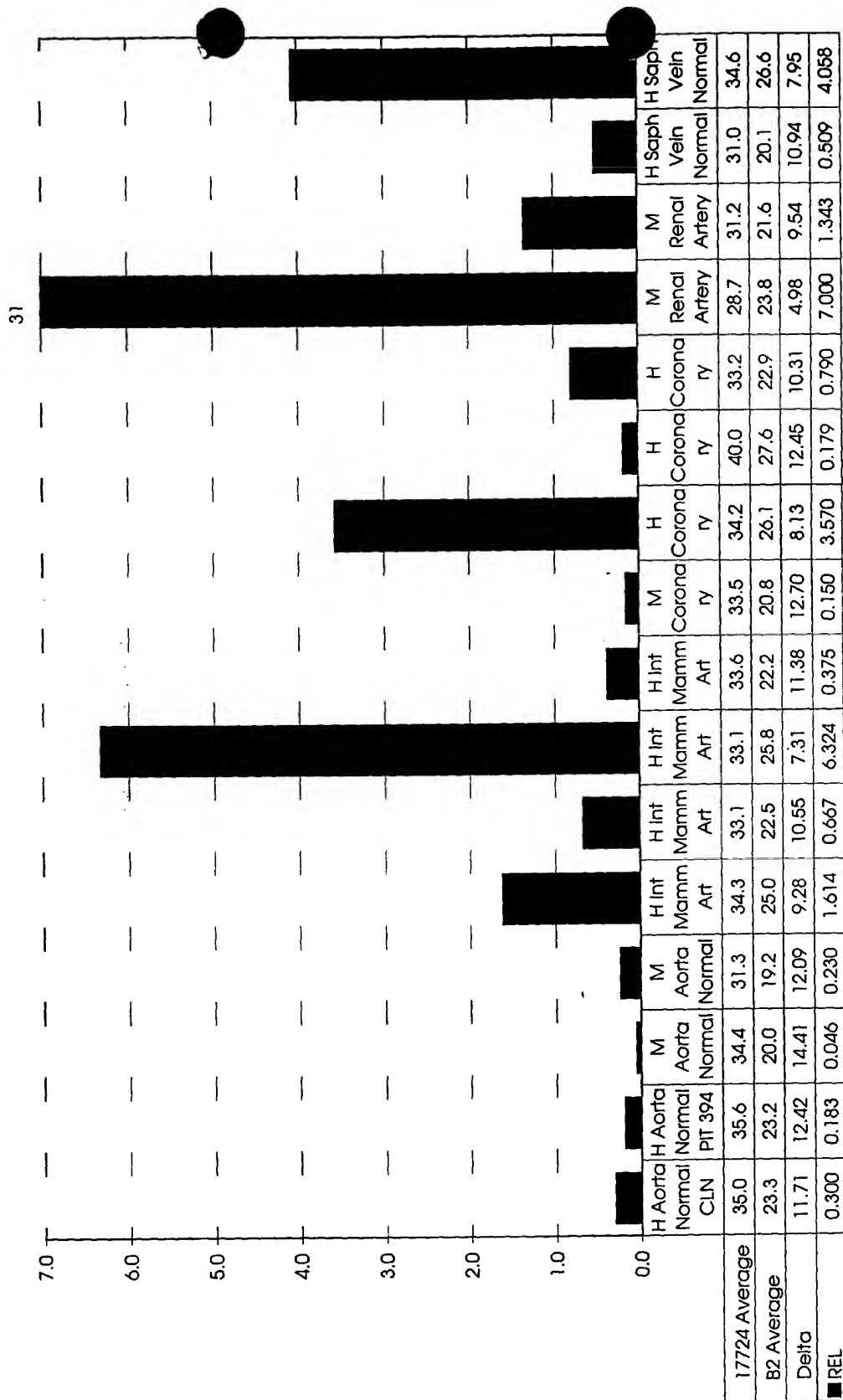


FIG. 7

Phase 1.2.1 expression of 17724



Analysis of 31945 (663 aa)

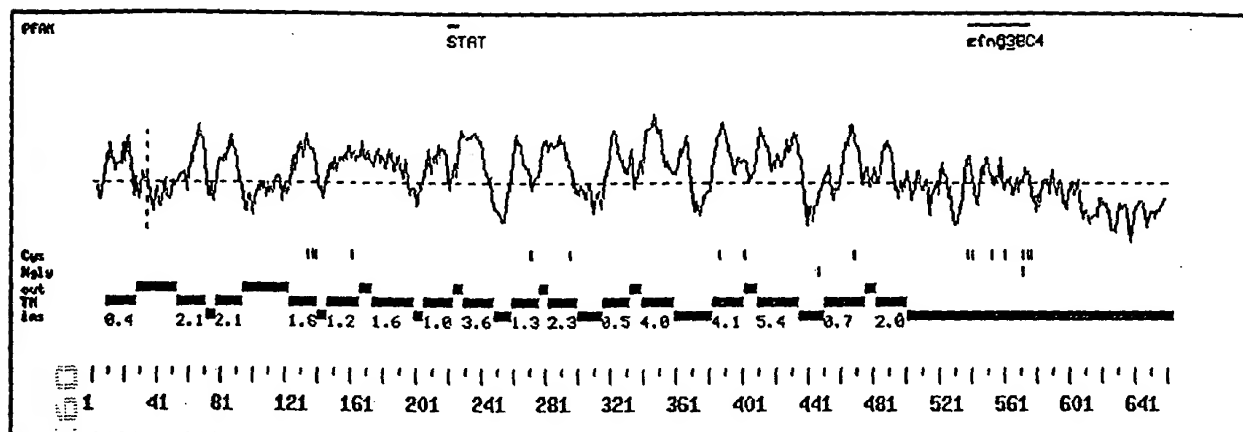


FIG. 9

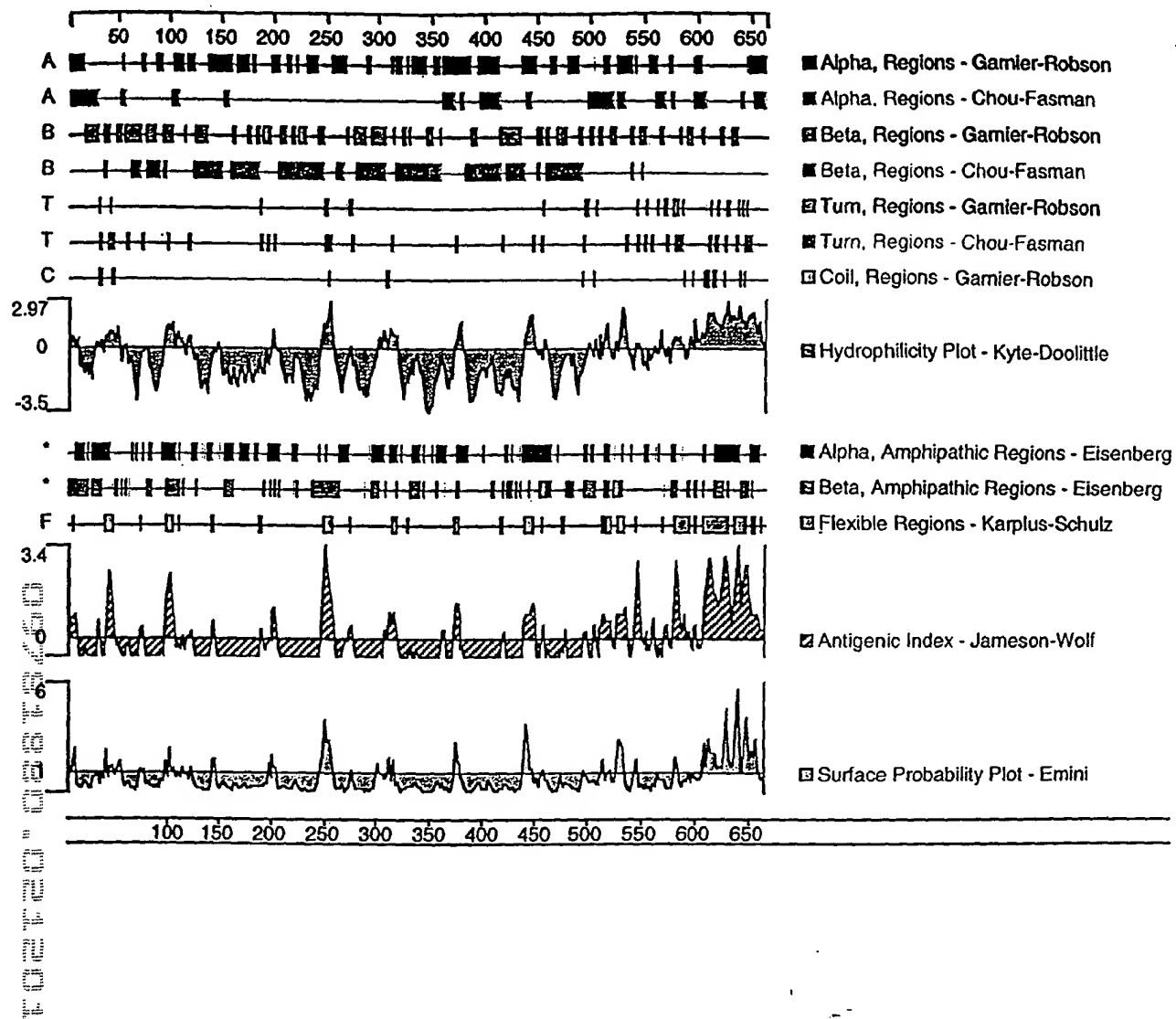
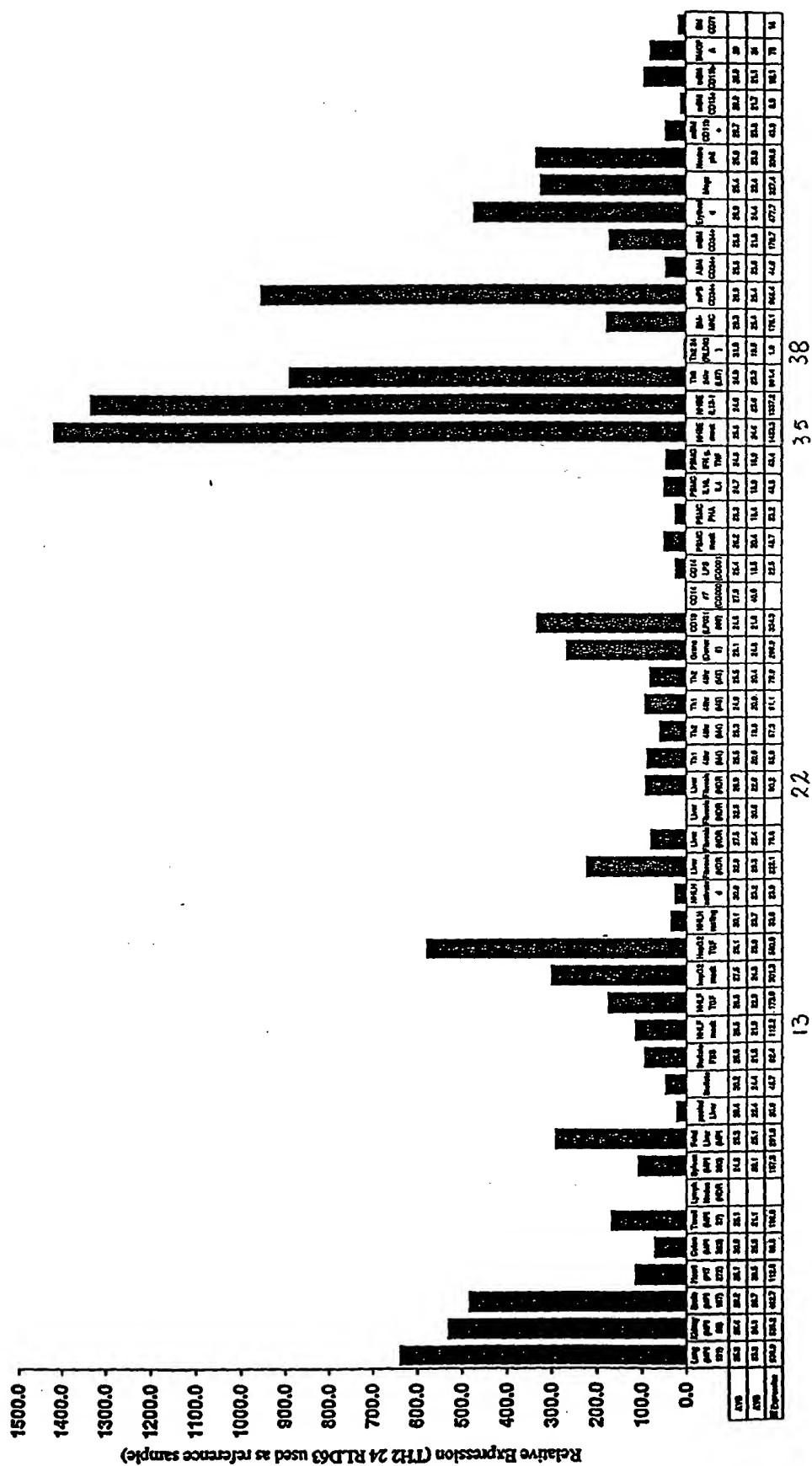
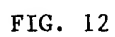


FIG. 10

Taqman Chart+Table

GPCR 31945 Expression



[illegible]

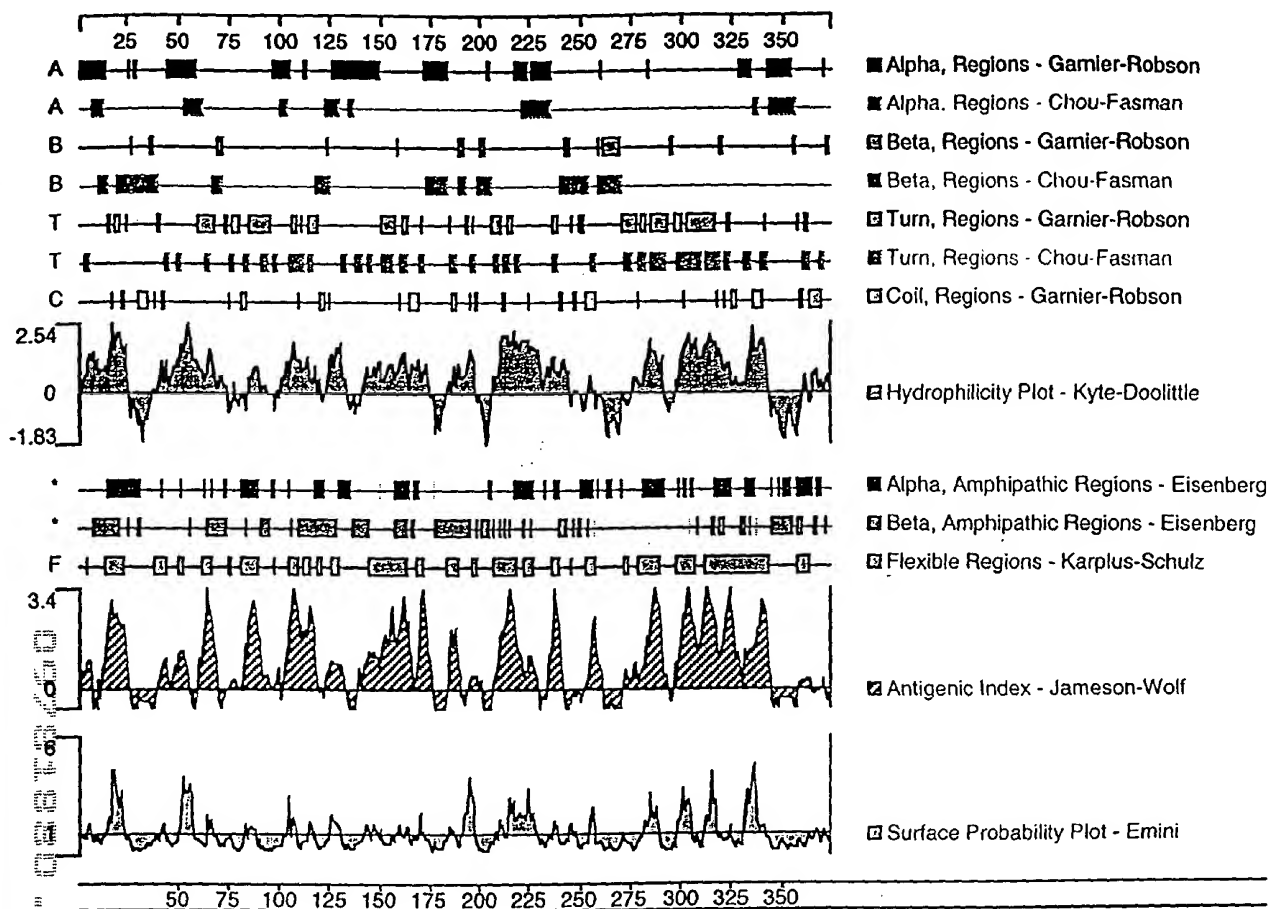


FIG. 13

SCANNED, # 6

Taqman Chart+Table

17724 GPCR Ph 1.9.1 Expression

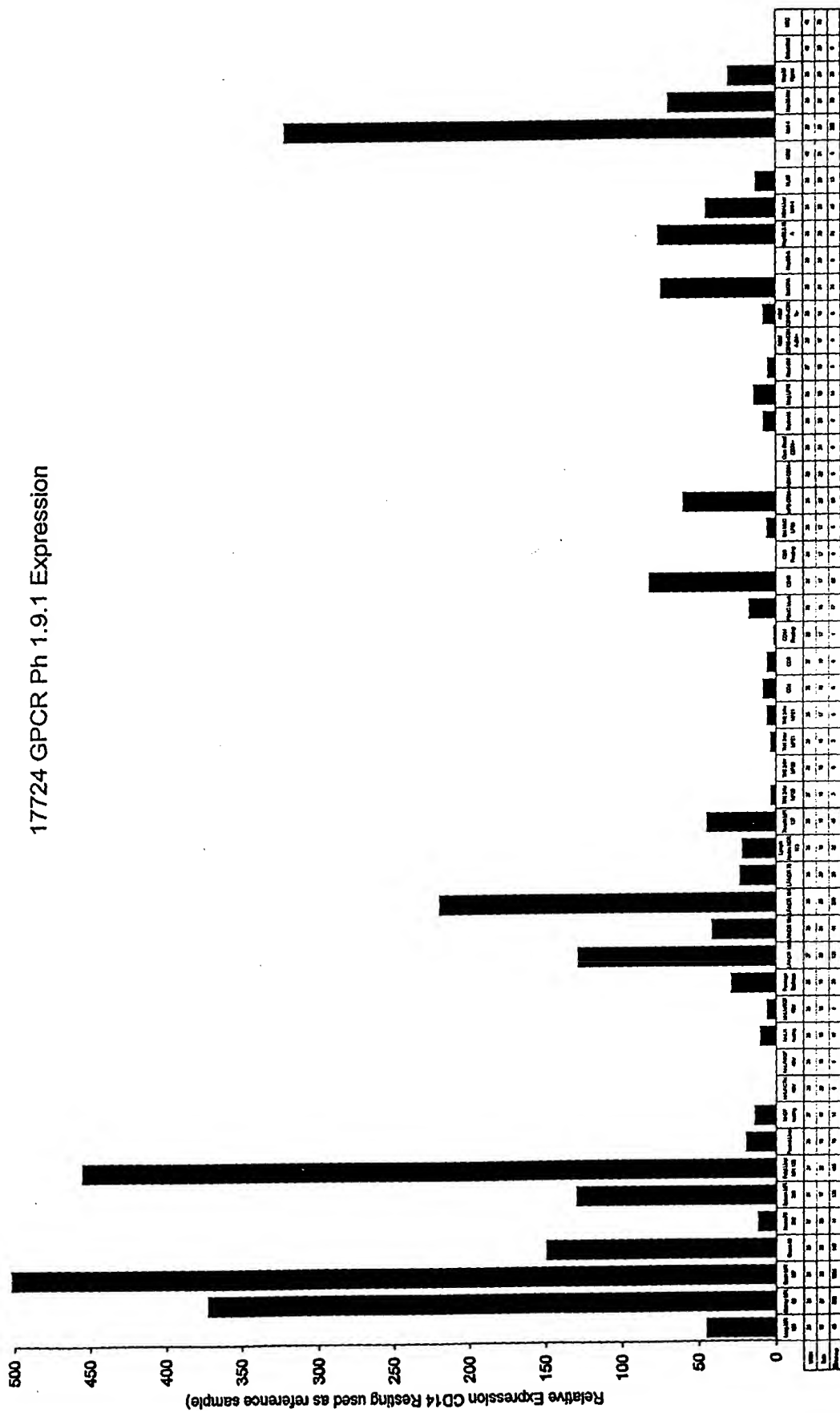
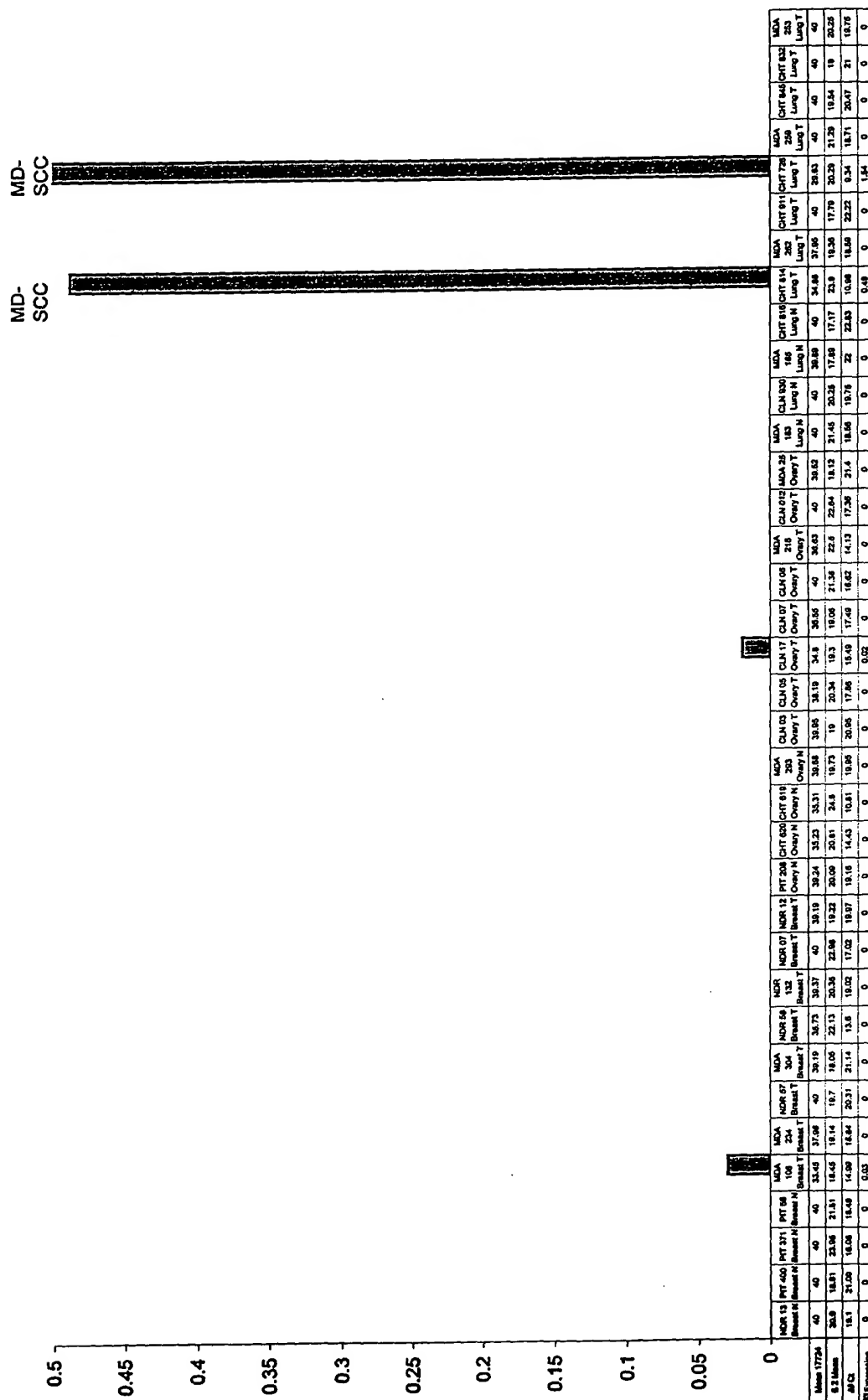


FIG. 14

SCANNED, # 6

17724 Expression in Oncology Plate I



SCANNED, #6

17724 CV II and III

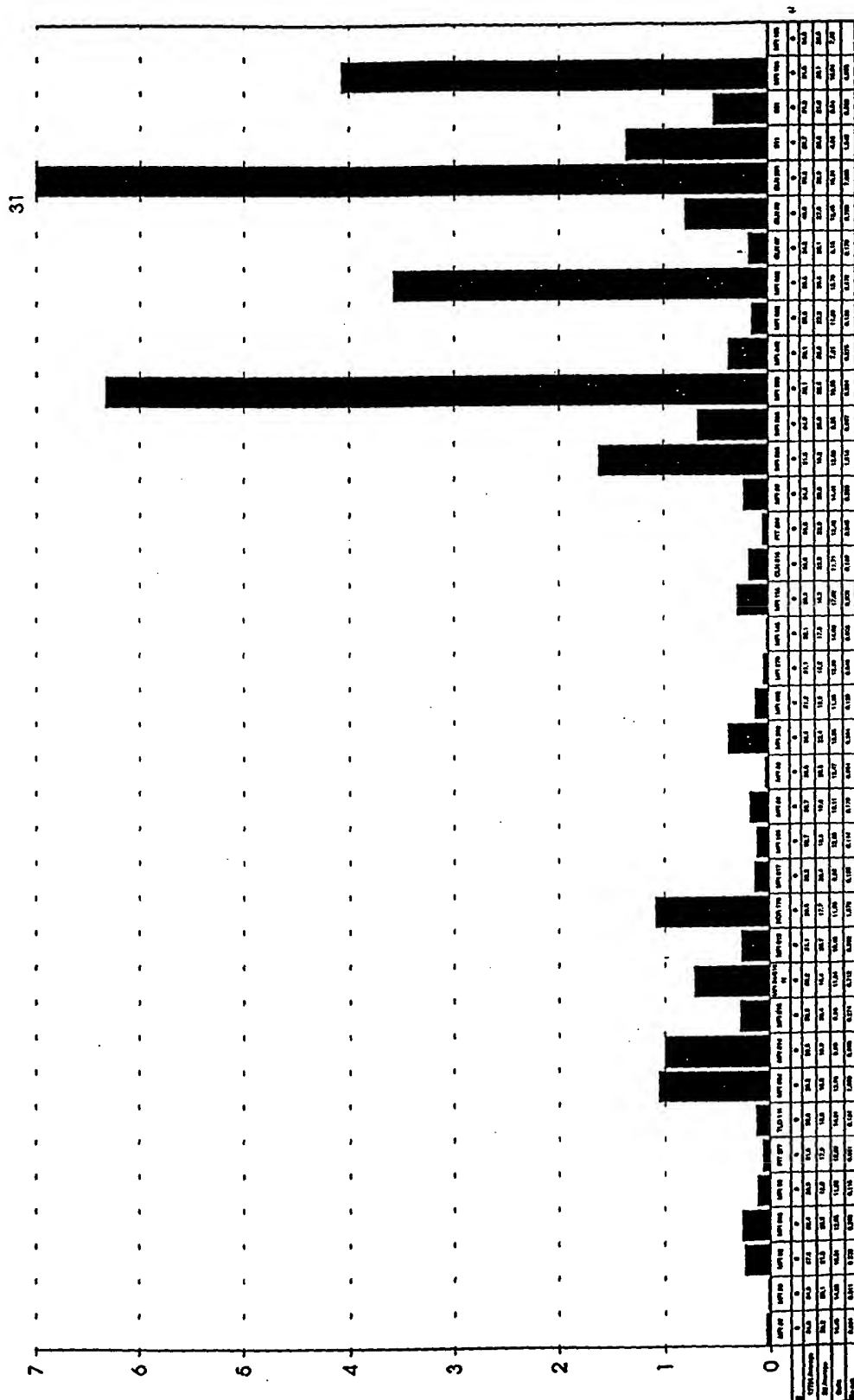


FIG. 16

CI ne cbhTb018f11jt

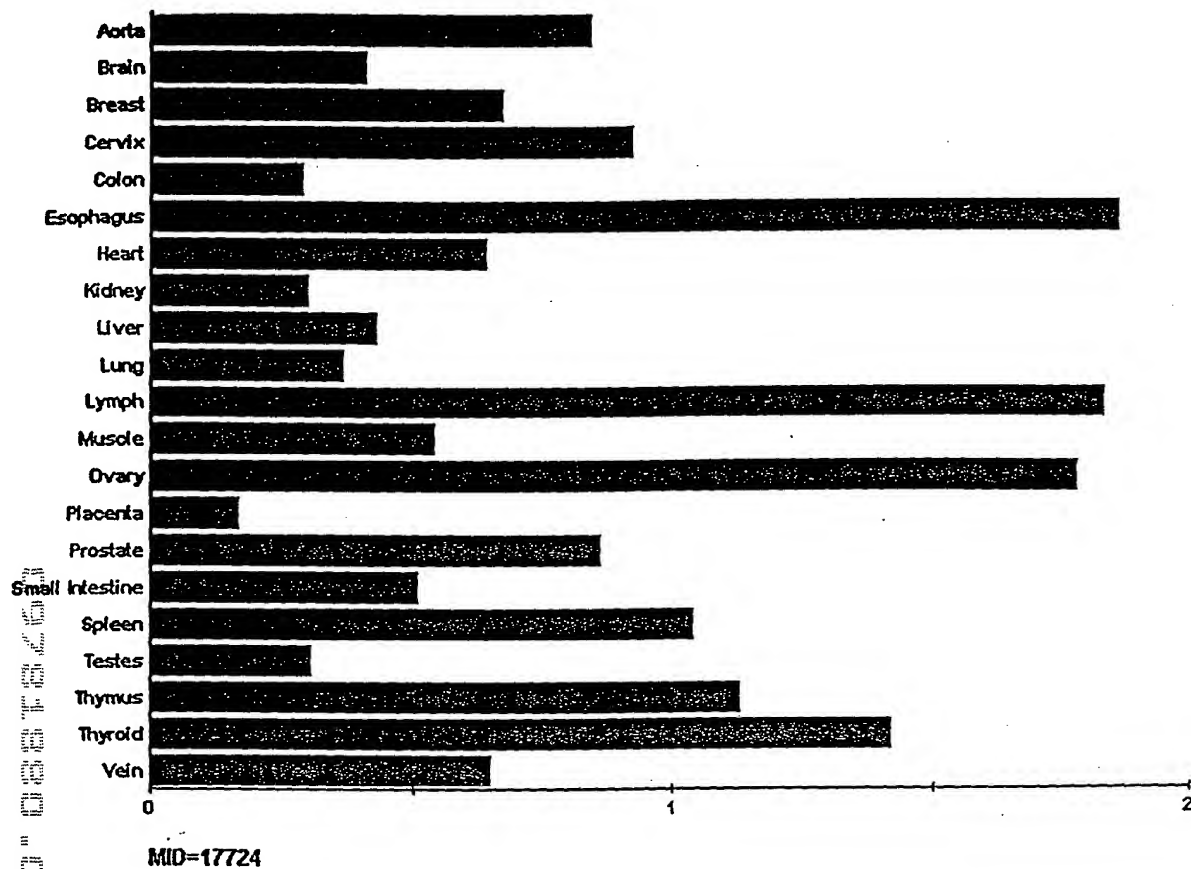


FIG. 17